

ABSTRACT

The present invention concerns methods and systems for analysis of drug resistance in
5 HIV-1. More specifically, the invention provides methods for predicting drug
resistance by correlating genotypic information with phenotypic profiles. The methods
allow the identification of primary and secondary resistance-associated mutations for
new and existing drugs and for calculating the contribution of mutations and
combinations of mutations to resistance and hyper-susceptibility. The invention allows
10 the design, optimization and assessment of the efficiency of a therapeutic regimen
based upon the genotype of the disease affecting a patient